

PCT09

RAW SEQUENCE LISTING

DATE: 10/11/2001

PATENT APPLICATION: US/09/701,121

TIME: 09:54:28

Input Set : A:\JH98K008.APP.txt

Output Set: N:\CRF3\10112001\I701121.raw

3 <110> APPLICANT: Hoechst Marion Roussel
 5 <120> TITLE OF INVENTION: Novel monomer protein with bone morphogenetic activity
 6 and medicinal agent containing the same for preventing
 7 and treating diseases of cartilage and bone.
 9 <130> FILE REFERENCE: JH98K008 PCT SEQUENCES IN ENGLISH
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/701,121 *OK*
 C--> 12 <141> CURRENT FILING DATE: 2000-11-20
 14 <150> PRIOR APPLICATION NUMBER: 10-141379
 15 <151> PRIOR FILING DATE: 1998-05-22
 17 <160> NUMBER OF SEQ ID NOS: 4
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 357
 23 <212> TYPE: DNA
 24 <213> ORGANISM: HUMAN
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1)..(357) *OK*
 29 <223> OTHER INFORMATION: Relevant amino acid residues in SEQ ID NO 1 from 1
 30 to 82 and from 84 to 119 in WO 95/04819.
 31 Note : aminoacid residue 83 is alanine *OK*
 32 instead of cysteine.
 34 <300> PUBLICATION INFORMATION:
 35 <301> AUTHORS: HOTTEN, Gertrud
 36 NEIDHARDT, Helge
 37 PAULISTA, Michael
 38 <302> TITLE: New growth/differentiation factor of the tgfbeta
 39 familie.
 40 <310> PATENT DOC NO: WO 95/04819
 41 <311> PATENT FILING DATE: 1995-02-16 *OK*
 43 <400> SEQUENCE: 1
 44 cca cta gca act cgt cag ggc aag cga ccc agc aag aac ctt aag gct 48
 45 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
 46 1 5 10 15
 48 cgc tgc agt cgg aag gca ctg cat gtc aac ttc aag gac atg ggc tgg 96
 49 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
 50 20 25 30
 52 gac gac tgg atc atc gca ccc ctt gag tac gag gct ttc cac tgc gag 144
 53 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
 54 35 40 45
 56 ggg ctg tgc gag ttc cca ttg cgc tcc cac ctg gag ccc acg aat cat 192
 57 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
 58 50 55 60
 60 gca gtc atc cag acc ctg atg aac tcc atg gac ccc gag tcc aca cca 240
 61 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
 62 65 70 75 80
 64 ccc acc gcc tgt gtg ccc acg cga ctg agt ccc atc agc atc ctc ttc 288

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65 Pro Thr Ala Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
66          85          90          95
68 att gac tct gcc aac aac gtg gtg tat aag cag tat gag gac atg gtc 336
69 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
70          100          105          110
72 gtg gag tcg tgt ggc tgt agg 357
73 Val Glu Ser Cys Gly Cys Arg
74          115
77 <210> SEQ ID NO: 2
78 <211> LENGTH: 119
79 <212> TYPE: PRT
80 <213> ORGANISM: HUMAN
82 <400> SEQUENCE: 2
83 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
84 1          5          10          15
86 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
87          20          25          30
89 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
90          35          40          45
92 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
93          50          55          60
95 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
96 65          70          75          80
98 Pro Thr Ala Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
99          85          90          95
101 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
102          100          105          110
104 Val Glu Ser Cys Gly Cys Arg
105          115
108 <210> SEQ ID NO: 3
109 <211> LENGTH: 39
110 <212> TYPE: DNA
111 <213> ORGANISM: HUMAN
113 <220> FEATURE:
114 <221> NAME/KEY: misc_feature
115 <222> LOCATION: (1)..(39) OK
116 <223> OTHER INFORMATION: Sense PCR primer for mutation introducing.
118 <400> SEQUENCE: 3
119 catgccatgg accccgagtc cacaccaccc accgcctgt 39
122 <210> SEQ ID NO: 4
123 <211> LENGTH: 37
124 <212> TYPE: DNA
125 <213> ORGANISM: HUMAN
127 <220> FEATURE:
128 <221> NAME/KEY: misc_feature
129 <222> LOCATION: Complement((1)..(37)) OK
130 <223> OTHER INFORMATION: Reverse PCR primer for mutation introducing.
132 <400> SEQUENCE: 4
133 cccaagcttg catgcctgcc ggtcgactac ctacagc 37

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date